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FIG. 1A

1 CGGACGCGTGGGCGCGCAGCCTGGCTGACCTGATCCTGGACCAGTGCCCCGACCGCGGCG 60

61 CGCCGGTGCCGCGAGATGCTGGCCCAGCCGCGAGCGGCTGCTCTTCATCCTGGACGGCGCGG 120  
1 M Q A Q P Q R L Q F I L D G A D 16

121 ACGAGCTGCCGGCGCTGGGGGGCCCCGAGGCCGCGCCCTGCACAGACCCCTTCGAGGCGG 180  
17 E L P A L G G P E A A P C T D P F E A A 36

181 CGAGCGGCGCGGGTGCTAGGCGGGCTGCTGAGTAAGGCGCTGCTGCCACGGCCCTCC 240  
37 S G A R V Q G G Q Q S K A L Q P T A L L 56

241 TGCTGGTGACACGCGCGCCGCCCGGGAGGCTGCAGGGCCGCTGTGTCCCCGC 300  
57 Q V T T R A A A P G R Q Q G R L C S P Q 76

301 AGTGCGCGGAGGTGCGCGGCTTCTCCGACAAGGACAAGAAGAAGTATTTCTACAAGTTCT 360  
77 C A E V R G F S D K D K K K Y F Y K F F 96

361 TCCGGGATGAGAGGAGGGCCGAGCGCGCTACCGCTTCGTGAAGGAGAACGAGACGCTGT 420  
97 R D E R R A E R A Y R F V K E N E T Q F 116

421 TCGCGCTGTGCTTCGTGCCCTTCGTGTGCTGGATCGTGTGCACCGTGCTGCGCCAGCAGC 480  
117 A Q C F V P F V C W I V C T V Q R Q Q L 136

481 TGGAGCTCGGTCCGGACCTGTGCGGCACGTCCAAGACCACCGTCAGTGCTACCTGCTTT 540  
137 E L G R D L S R T S K T T T S V Y Q L F 156

541 TCATCACCAGCGTTCTGAGCTCGGCTCCGGTAGCCGACGGGCCCCGGTTGCAGGGCGACC 600  
157 I T S V L S S A P V A D G P R L Q G D Q 176

601 TGGCAATCTGTGCCGCTGGCCCGCGAGGGCGTCCTCGGACGCAGGGCGCAGTTTGCCG 660  
177 R N Q C R Q A R E G V L G R R A Q F A E 196

661 AGAAGGAAC TGAGCAACTGGAGCTTCGTGGCTCCAAAGTGACAGACGCTGTTTCTCAGCA 720  
197 K E Q E Q L E L R G S K V Q T L F L S K 216

721 AAAAGGAGCTGCCGGGCGTGCTGGAGACAGAGGTCACCTACCAGTTCATCGACCAGAGCT 780  
217 K E L P G V L E T E V T Y Q F I D Q S F 236

781 TCCAGGAGTTCCTCGCGGCACTGTCTACCTGCTGGAGGACGGCGGGGTGCCAGGACCG 840  
237 Q E F L A A L S Y L Q E D G G V P R T A 256

841 CGGCTGGCGGCGTTGGGACACTCCTGCGTGGGGACGCCAGCCGCACAGCCACTTGGTG 900  
257 A G G V G T L Q R G D A Q P H S H L V L 276



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FIG. 1B

901	TCACCACGCGCTTCCTCTTCGGACTGCTGAGCGCGGAGCGGATGCGCGACATCGAGCGCC	960
277	T T R F L F G <u>I</u> L S A E R M R D I E R H	296
961	ACTTCGGCTGCATGGTTTCAGAGCGTGTGAAGCAGGAGGCCCTGCGGTGGGTGCAGGGAC	1020
297	F G <u>C</u> M V S E R V K Q E A L R W V Q G Q	316
1021	AGGGACAGGGCTGCCCCGAGTGGCACCAGAGGTGACCGAGGGGGCCAAAGGGCTCGAGG	1080
317	G Q G C P G V A P E V T E G A K G L E D	336
1081	ACACCGAAGAGCCAGAGGAGGAGGAGGAGGAGGCCCAACTACCCACTGGAGTTGC	1140
337	T E E P E E E E E G E E P N Y P L E L <u>I</u>	356
1141	TGTACTGCCTGTACGAGACGCAGGAGGACGCGTTTGTGCGCCAAGCCCTGTGCCGGTTCC	1200
357	Y <u>C</u> <u>I</u> Y E T Q E D A F V R Q A L C R F P	376
1201	CGGAGCTGGCGCTGCAGCGAGTGCCTTCTGCCGCATGGACGTGGCTGTTCTGAGCTACT	1260
377	E L A L Q R V R F C R M D V A V L S Y <u>C</u>	396
1261	GCGTGAGGTGCTGCCCTGCTGGACAGGCACTGCGGCTGATCAGCTGCAGATTGGTTGCTG	1320
397	V R C C P A G Q A L R <u>I</u> I S C R L V A A	416
1321	CGCAGGAGAAGAAGAAGAGCCTGGGGAAGCGGCTCCAGGCCAGCCTGGGTGGCGCA	1380
417	Q E K K K K S <u>I</u> G K R L Q A S L G G G S	436
1381	GTTCTCAAGGCACCACAAAACAAGTCCAGCCTCCCTTCTTCATCCACTCTTTCAGGCAA	1440
437	S Q G T T K Q <u>I</u> P A S L L H P L F Q A M	456
1441	TGACTGACCCACTGTGCCATCTGAGCAGCCTCACGCTGTCCCACTGCAAACCTCCCTGACG	1500
457	T D P L <u>C</u> H <u>I</u> S S L T L S H C K L P D A	476
1501	CGGTCTGCCGAGACCTTTCTGAGGCCCTGAGGGCAGCCCCGCACTGACGGAGCTGGGCC	1560
477	V C R D L S E A <u>I</u> R A A P A L T E <u>I</u> G <u>I</u>	496
1561	TCCTCCACAACAGGCTCAGTGAGGCGGGACTGCGTATGCTGAGTGAGGGCCTAGCCTGGC	1620
497	L H N R L S E A G L R M <u>I</u> S E G L A W P	516
1621	CGCAGTGCGGGTGCAGACGGTCAGGGTACAGCTGCCTGACCCCCAGCGAGGGCTCCAGT	1680
517	Q <u>C</u> R V Q T V R V Q L P D P Q R G L Q Y	536
1681	ACCTGGTGGGTATGCTTCGGCAGAGCCCCGCCCTGACCACCTGGATCTCAGCGGCTGCC	1740
537	<u>I</u> V G M <u>I</u> R Q S P A <u>I</u> T T L D <u>I</u> S G C Q	556
1741	AACTGCCCCGCCCCATGGTGACCTACCTGTGTGCAGTCCTGCAGCACCAGGGATGCGGCC	1800
557	<u>I</u> P A P M V T Y <u>I</u> C A V <u>I</u> Q H Q G <u>C</u> G <u>I</u>	576

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FIG. 2A-1

		1		50
HLRRII1		(1)	-----	
caspase_recruitment_protein		(1)	MAGGAWGR <del>L</del> ACYLE <del>F</del> FLKK <del>E</del> ELKE <del>F</del> Q <del>L</del> LLANKA <del>H</del> SRSSSGE <del>T</del> PAQPEK <del>T</del> SG	
cryopyrin		(1)	-MASTRCK <del>L</del> ARYLED <del>E</del> EDV <del>D</del> LKKF <del>K</del> MH <del>L</del> ED <del>V</del> PPQ <del>K</del> GCIP <del>L</del> PRG <del>O</del> TEKADH	
Nucleotide_Binding_site		(1)	----MGFN <del>L</del> QALL <del>E</del> Q <del>L</del> SQ <del>D</del> EL <del>S</del> KFKYL <del>L</del> TTT <del>S</del> PA <del>H</del> ELQ <del>K</del> TPHKE <del>F</del> VD <del>K</del> ADG	
		51		100
HLRRII1		(1)	-----	
caspase_recruitment_protein		(51)	MEVAS <del>L</del> YLAQYCE <del>Q</del> RAW <del>D</del> EA <del>L</del> H <del>T</del> WE <del>Q</del> MLR <del>S</del> LCAQ <del>A</del> Q <del>E</del> GAGH <del>S</del> PSFP <del>Y</del> SP	
cryopyrin		(50)	VDLA <del>T</del> EM <del>I</del> DFNGEE <del>K</del> AWA <del>M</del> AV <del>T</del> FAA <del>T</del> NR <del>R</del> DL <del>Y</del> EKA <del>R</del> DEPKW <del>C</del> SDNARV	
Nucleotide_Binding_site		(47)	KOL <del>V</del> E <del>L</del> L <del>T</del> THC <del>D</del> SYW <del>V</del> EMAS <del>L</del> Q <del>V</del> FEK <del>M</del> HR <del>M</del> DLSE <del>R</del> AK <del>D</del> EVREA <del>L</del> K <del>S</del> ENK	
		101		150
HLRRII1		(1)	-----	
caspase_recruitment_protein		(101)	SEPHLGSPSQPTSTAVLMPWIHELPA <del>G</del> CTQGSERRVLRQLPDTSGRRWRE	
cryopyrin		(100)	SN-----	
Nucleotide_Binding_site		(97)	RK-----	





**FIG. 2A-2**

		151		200
HLRRSI1		(1)	-----	-----
caspase_recruitment_protein		(151)	ISASHLYQALPSSPDHESPSQESPNAPTSTAVLGSWGSPQP	PSTAPRQE
cryopyrin		(102)	-----	PVTCQEDS
Nucleotide_Binding_site		(99)	-----	PLSGITR-
		201		250
HLRRSI1		(1)	-----	-----
caspase_recruitment_protein		(201)	APGTQWPLDETSGIYITEIREREREKSEKGRPPMAA	VGVTPPAHSSLP
cryopyrin		(111)	IIEEWGLLEYLSRLSICKMKDYRKKYRYVRSRFQCIEDRNARLGESV	
Nucleotide_Binding_site		(107)	KERPPIVDDEMLEREKTEAQDKDNRCRYILTKFERMWSWP	PGDSKEVQV
		251		300
HLRRSI1		(1)	-----	-----
caspase_recruitment_protein		(251)	HHPHMEPSVRESLCSTWPWKNEDEFNQFTQLLLLRPHPRSQDPLVKRSW	
cryopyrin		(161)	SLNKRYSRIRLIKEHRSQQEREQELLAI GKTKTCESPV	
Nucleotide_Binding_site		(157)	MAERYKMLIPFSNPR	-----

FIG. 2A-3

		301			350
		(1)	-----	-----	
HLRRSI1		(301)	PDYVEENRGHIEIRDLFGPGIDIQEPRIVTLLOGAAGIGKSTLARQVKEA		
caspase_recruitment_protein		(199)	-----SPDKMELLFDPPDDEHSEPVETVVFFQGAAGIGKTI LARKMMLD		
cryopyrin		(172)	-----	-----VLPQPFSTVTVLLYGPAGLGKTTLAQKLMLD	
Nucleotide_Binding_site					
		351			400
		(1)	-----	-----MLA	
HLRRSI1		(351)	WCRGOLYCDRFQHVFFYSCRELAQSKVVSIAELIGKDGATATPAPTRQILS		
caspase_recruitment_protein		(241)	WASGTLYQDRFDYLFYTHCREVSLVTQRSICDLIMSCCPDPNPPHKKIVR		
cryopyrin		(202)	WAEDNLIHK-FKYAFYLSCRELSRLGPCSEAEVFRDWPELQDDIPHLLA		
Nucleotide_Binding_site					
		401			450
		(4)	OPQRLFLILDGADELP-ALGCPFAAPCTDPFAAGCARVLGGLISKALLP		
caspase_recruitment_protein		(401)	RPERLFLILDGVDEPGWVLOEPSSELCLLWSQPQPADALLGSLLCGKTLPL		
cryopyrin		(291)	KPSRLFLIMDGFDELOGAEDDEHIGPLCTDWQKAERGDILLSSILRRKKLLP		
Nucleotide_Binding_site		(251)	QARKQLFWVIDGFDLGAAPGALLIEDICGDWEKKKPVVLLGSLINRVMLP		



FIG. 2A-4

HLRRSI1	451	(53)	TALLVTTTRAAAPGRLQGRLCSPQCAEVRGFSDDKKKYFYKFFRDERRA	500
caspase_recruitment_protein		(451)	EASLLTARITATQNLIPSEQARWVEVLGFSESSRKEYFYRYFTDERQA	
cryopyrin		(341)	EASLLTTRPVALEKQLQLLDHPRHVE LGFSEAKRKEYFFKYFSDQAQA	
Nucleotide_Binding_site		(301)	KALLVTRPRALRDLRIIAEEPVYTRVEGFLEEDKRAYFLRHFGDEDDQA	
HLRRSI1	501	(103)	ERAVREVKENETLFALCFVPVCWIVCTVLRQQLELGRDLSRTSKTTTSV	550
caspase_recruitment_protein		(501)	IRAFRLVKSNEKELWALCVPWVSWLACTCLMQQMKRKEKLILTSKTTTTL	
cryopyrin		(391)	RAAFSLIOENEVLFIMCFPIVCWIVCTGLKQOMESGKSLAQTSKTTTAV	
Nucleotide_Binding_site		(351)	MRAFEIMRSNAALFQLGSAPAVCWIVCTTLKLQMEKGEDPVPTCLTRTGL	
HLRRSI1	551	(153)	YLLFLTSTVLSAPVADGPRLQGLRNLCRLAREGVLCRRAQFAEKELHQL	600
caspase_recruitment_protein		(551)	CLHMLAQALQAQP-----LGPQLRDLCSLAAEGIWOKKLFSPDDLRLKH	
cryopyrin		(441)	YVFFLSSILQPRGGQEHGLCAHLWGLCSLAADGIMNQKILFFESDILRNH	
Nucleotide_Binding_site		(401)	FLRFLCSREP-----QGAQLRGALRTLSSLAAQGLWAQTSVLRHREDLERI	



HLRSI1	(203)	ELRGSKVOTLEFLSKKELPGVLETEVTYQFIDQSFQEF AALSYLLEDGGV	601	650
caspase_recruitment_protein	(595)	GLDCAIISTFLKMG--ILQEHPIPLSYSFIHLQFQEFFAAMSYVLEDEK-		
cryopyrin	(491)	GLQKADVSAFLRMN-LEQKEVDCEKFSFIHMTFQEFFAAMYLLLEEKEK		
Nucleotide_Binding_site	(446)	GVQESDILRLFLDGD-ILRQDRVSKGYSFIHLSFQCFLLALFYTLLEKEEE		
HLRSI1	(253)	PTAAAG-----VGTLLRGDAQPHSLVLTTTRFLFGLLSAERMMD	651	700
caspase_recruitment_protein	(642)	-----GRGKHSNCIIDLEKTEAAYGTHGLFGASTTRFLFGLLSDEGERE		
cryopyrin	(540)	GRTNVPGSRILKLPSRDVIVLLENYCKFEKGYLIFVVRFLFGLVNCERTSY		
Nucleotide_Binding_site	(495)	EDRDGHTWDIG----DVQKLLSGVERLRNPDLIQAGYSEGLANEKRAKE		
HLRSI1	(293)	TERHFGCMVSEIRVKQEA LRWVQCGQGCGPVAPEVTEGAKGLEDTTEEPPE	701	750
caspase_recruitment_protein	(686)	MENIFHCRLSQ--GRNLQMOWVPSL-----QLLLQPHS-----		
cryopyrin	(590)	LEKKLSCKTISQIRLELLKWI EVK-----AKAKKLLQIQPSQ		
Nucleotide_Binding_site	(541)	LEATFGCRMSPDIKQELLRCDISC-----KGGHSTVTDLQ		



FIG. 2B-2

		751			800
HLRRSI1		(343)	EEEEEPNYP	LELLYCLYETQEDAFVRQALCRFPETALQ	RVRFRCRMDVAV
caspase_recruitment_protein		(716)	-----	LESLHCLYETRNKTFLLTQVMAHFEEMGMC--	VEITDMFLLLV
cryopyrin		(626)	-----	LELFYCLYEMQEEDEVRAMDYFPKIEIN--	LESTRMDHVV
Nucleotide_Binding_site		(576)	-----	ELLGCLYESQEEELVKEVMAQFKELSLH---	LNAVDMVP
		801			850
HLRRSI1		(393)	LSYCVRC	CPAGQALRLISCRLLVAAQEKKKKSLGKRLQASL	CGGSSQ----
caspase_recruitment_protein		(754)	CTFCIKF	SRHVKKLQLEGRQHRSTWSPSMVVLFRWVP	VTDAYWQILFS-
cryopyrin		(664)	SSFCTEN	CHRVESLSLGFJHNMPEEEEEKEGRLDMVQCV	LPSSSHAA
Nucleotide_Binding_site		(612)	SSFQV	KHCRNTQKMSLQVTKENLPENVTA	SESDAEVERSQDDQHMPFWT
		851			900
HLRRSI1		(439)	-----	-----	-----
caspase_recruitment_protein		(803)	-----	-----	-----
cryopyrin		(714)	CSHG	VN <del>SH</del> -----	-----
Nucleotide_Binding_site		(662)	DLCS	FGSNKDLMGLAINDSFLSASLVRILCEQIASDTCHLQ	RVVFKNIS



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FIG. 2B-3



		901		950
HLRSI1		(439)	-----GTTKQLPASLLEPLFOAMTDPPLCHLSLT	
caspase_recruitment_protein		(803)	-----VLKVRNLIKELDSCNSLSHSAVKSLSCKTLRRPRCLLETLR	
cryopyrin		(725)	SSFCRGLFSLSTQSLTELDLSDNSLGDPGMRVLCETLOHPGCNIRRLW	
Nucleotide_Binding_site		(712)	PAADHRNLCTALRGHKTVTYLTLCNDQDDMFPAALCEVLRHPECNIRVLG	
		951		1000
HLRSI1		(468)	LSHCKIIPDAVCPDLSEALRAAPALTTELGLLENRLSEAGLRMLSEGLAWPQ	
caspase_recruitment_protein		(844)	LACGLTAEDCKDLAFCGLRANQITLTELDSLNFVLM DAGAKHLCQRLRQPS	
cryopyrin		(775)	LCRCGLSHECCFDISLVLSNQKIVELDLSDNALGDFGIRLLCVGLKHLL	
Nucleotide_Binding_site		(762)	LVSCSATTOQWADLSLAEVNSQLTCVNLSDNELDEGAKLLYTTLRHPK	
		1001		1050
HLRSI1		(518)	CRVQTVRQQLPDPQ-RGLQYLVGMRLRQSPALTTLDSLSCQLPAPMVTYLC	
caspase_recruitment_protein		(894)	CKLQRLQLVSCGLTSDCCQDLASVLSASPSLKELDLQNNLDDVGVRLC	
cryopyrin		(825)	CNKKKLMVSCCLTSACCCDLASVLSLSTSHSLTRLVYGENALGDSGVAILC	
Nucleotide_Binding_site		(812)	CFLQRLSLENCHLTETANCKDLAAVLVVSRELTHCLAKNPICNTGVKFLC	

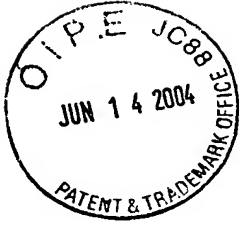
FIG. 2B-4



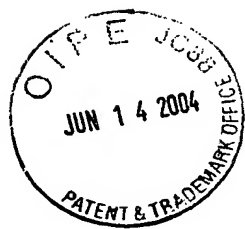
HLRRSI1	1051	1100
caspase_recruitment_protein	(567)	AVLQHQCGLQTLSLASVFLSEQSLQELQAVKRAKPDLMITTPALDGHPO
cryopyrin	(944)	EGLRHPACKLIRLGLDOTLSDVMRQELRALEQEKPOLLIERSRKPSVMT
Nucleotide_Binding_site	(875)	EKAQNPQCNLQKGLVNSGLTSVCCSALSSVLSITNQNLTHLYLRGNITLGD
	(862)	EGLRYPECKLQTLVLMNCDITSDGCCDLTKLLOEKSSLLCLDLGLNHIGV
HLRRSI1	1101	1150
caspase_recruitment_protein	(617)	PPKELITSTF-----
cryopyrin	(994)	PIEGLDTGEMSNSTSLKRRQLGSERAAASHVAQANLKLDDVSKIPIPIAEI
Nucleotide_Binding_site	(925)	KCHKLLCEGLLHPDCKLQVLELDNENITSHCCWDLSTLLTSQSILRKLISL
	(912)	KGMKELCEALRKPLCNLRCLWLWGCSTPPEFSCEDLCSALSN-QSLVTLIDL
HLRRSI1	1151	1200
caspase_recruitment_protein	(626)	-----
cryopyrin	(1044)	AEESSPEVVPVELLCVPSPAQSGDLHTKPLGTDDEFWGPTGPVATEVVDK
Nucleotide_Binding_site	(975)	CNN---DLGDLGVMMFCEVLKQSSCLLQNLGLSEMVFNYETKSALETLOE
	(961)	CQN---PLGSSGVKMLFETLTCCSSGTLRLRLKIDDFENDELNKLLEEEFE

**FIG. 2C-1**

		1201		1250
HLRRSI1	(626)	-----	-----	-----
caspase_recruitment_protein	(1094)	EKNLYR	VHEPVA	AGSRWPN
cryopyrin	(1022)	EKPELT	VVEEPQ	W-----
Nucleotide_Binding_site	(1008)	KNPQLI	TDTEK	HHPMAERP
				SHDFM
		1251		1300
HLRRSI1	(626)	-----	-----	-----
caspase_recruitment_protein	(1144)	SWMVAG	PLLDI	KAEPG
cryopyrin	(1035)	-----	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----	-----
		1301		1350
HLRRSI1	(626)	-----	-----	-----
caspase_recruitment_protein	(1194)	LEKPAR	VELHH	IVLEN
cryopyrin	(1035)	-----	-----	-----
Nucleotide_Binding_site	(1034)	-----	-----	-----
				PSPLG
				VLLK
				MIHN
				ALRF
				IPVT
				SVV
				LVLL
				YHRL
				HP



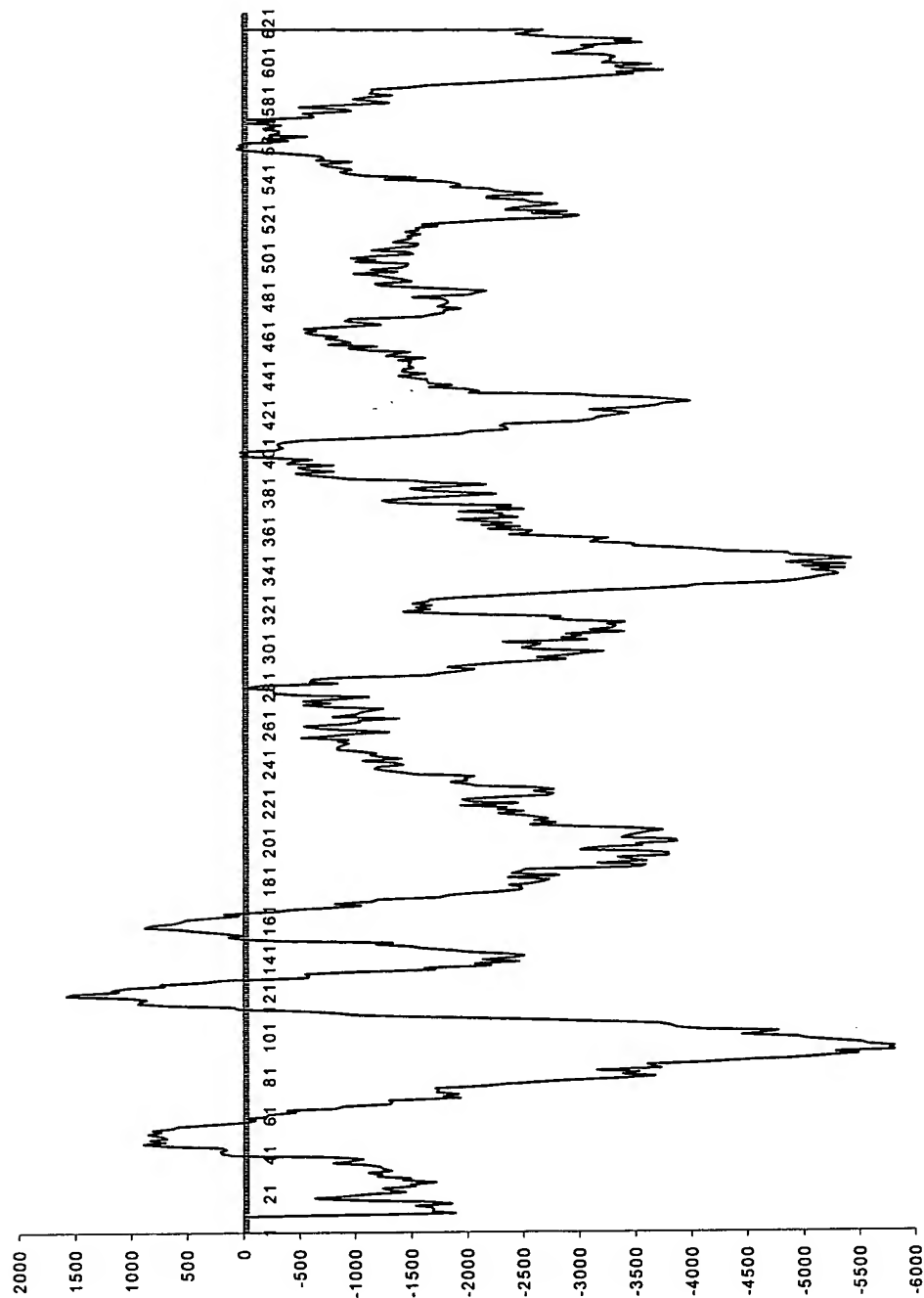
HLRRSI1	1351		1400
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1244)	EEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVGHLSGIRLQVK	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----
HLRRSI1	1401		1450
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1294)	DKKDETLVWEALVKPGDIMPATTLIPACIAVPSPLDAPQLLHFVDQYRE	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----
HLRRSI1	1451		1500
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1344)	QLIARVTSVEVVLDKLHGQVLSQEYERVLAEINTRPSQMRKLFSLSQSWD	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----
HLRRSI1	1501		1536
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1394)	RKCKDGLYQALKETHPHLIMELWEKSKKGLPLSS	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----



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FIG. 3

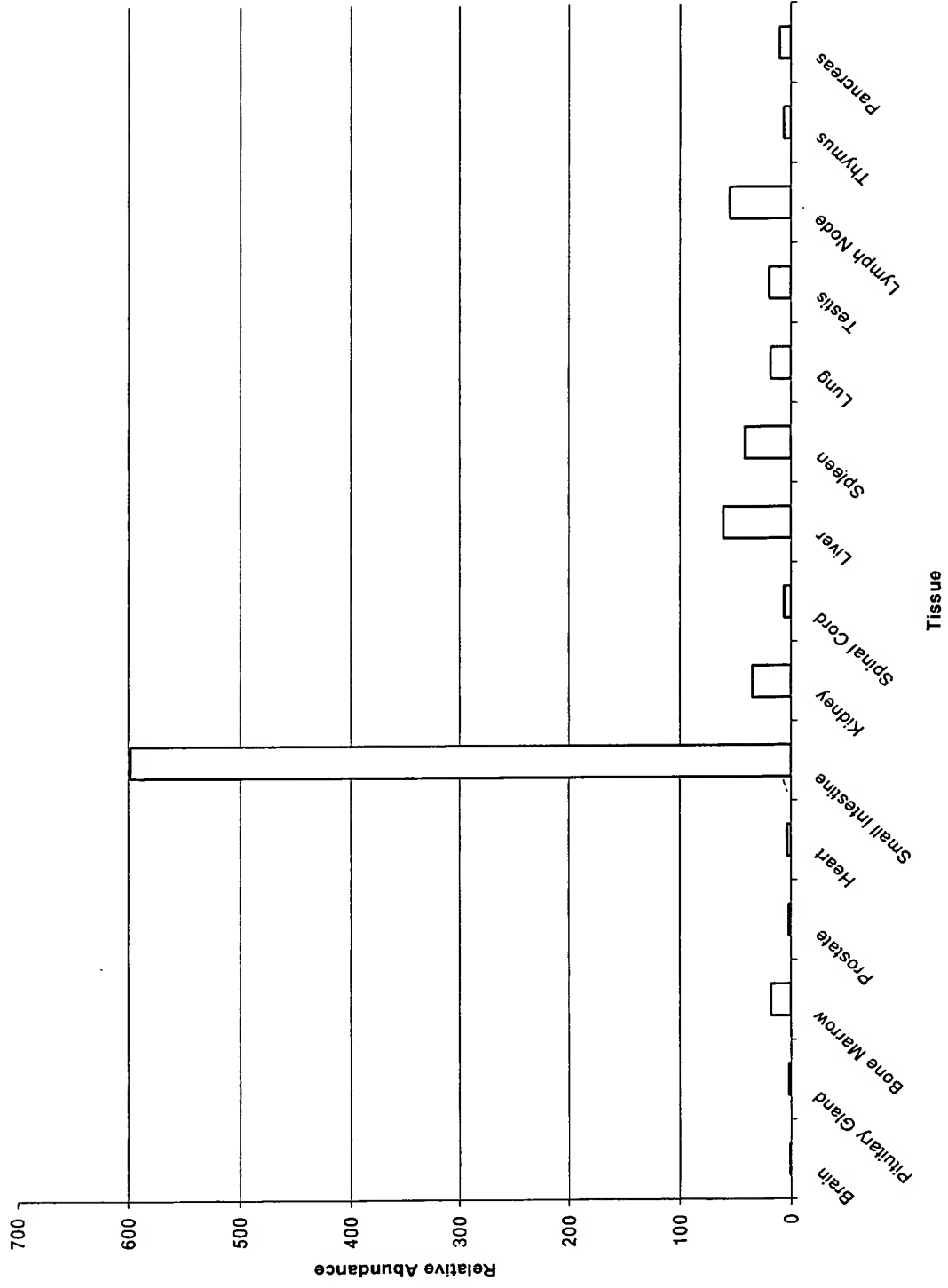


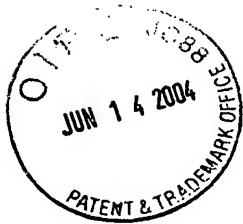


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FIG. 4





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**FIG. 5**

Protein	Genbank ID	Identities	Similarities
human caspase recruitment protein 7	gi 10198209	36.3%	44.0%
human nucleotide binding site protein	gi 10198207	35.0%	42.2%
human cryopyrin protein	gi 17027237	35.7%	46.0%